

FIG. 1

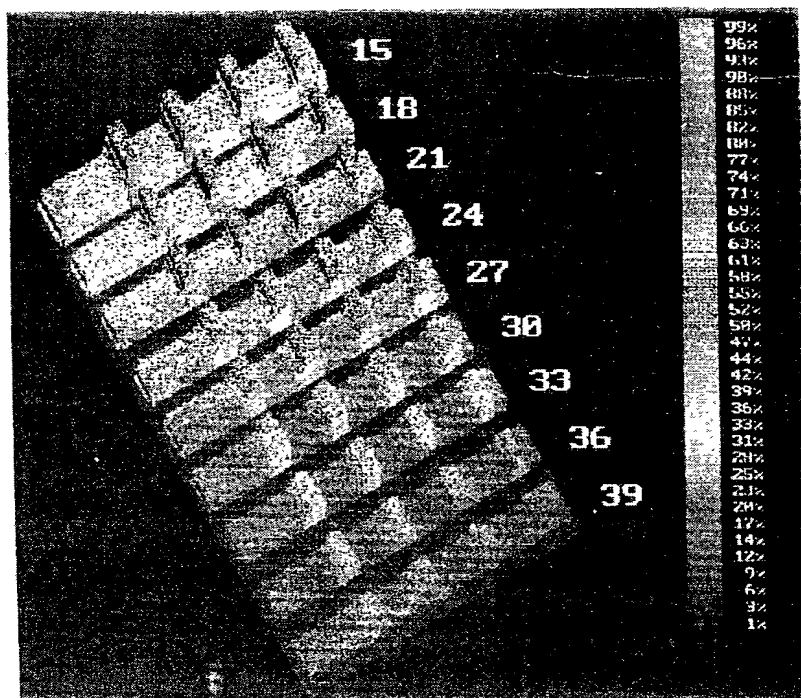


FIG. 2

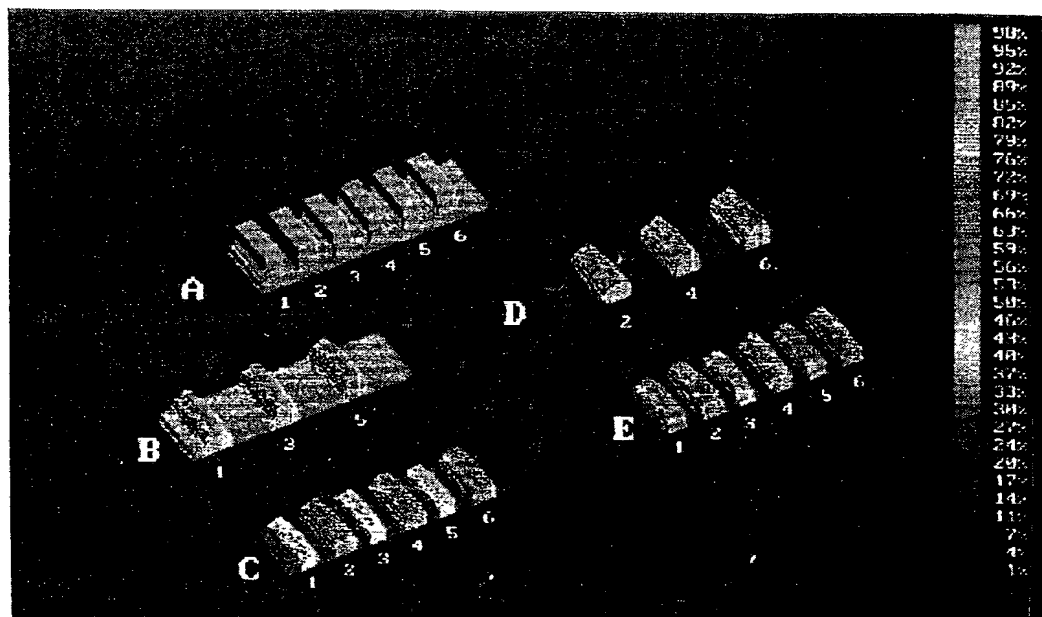


FIG. 3

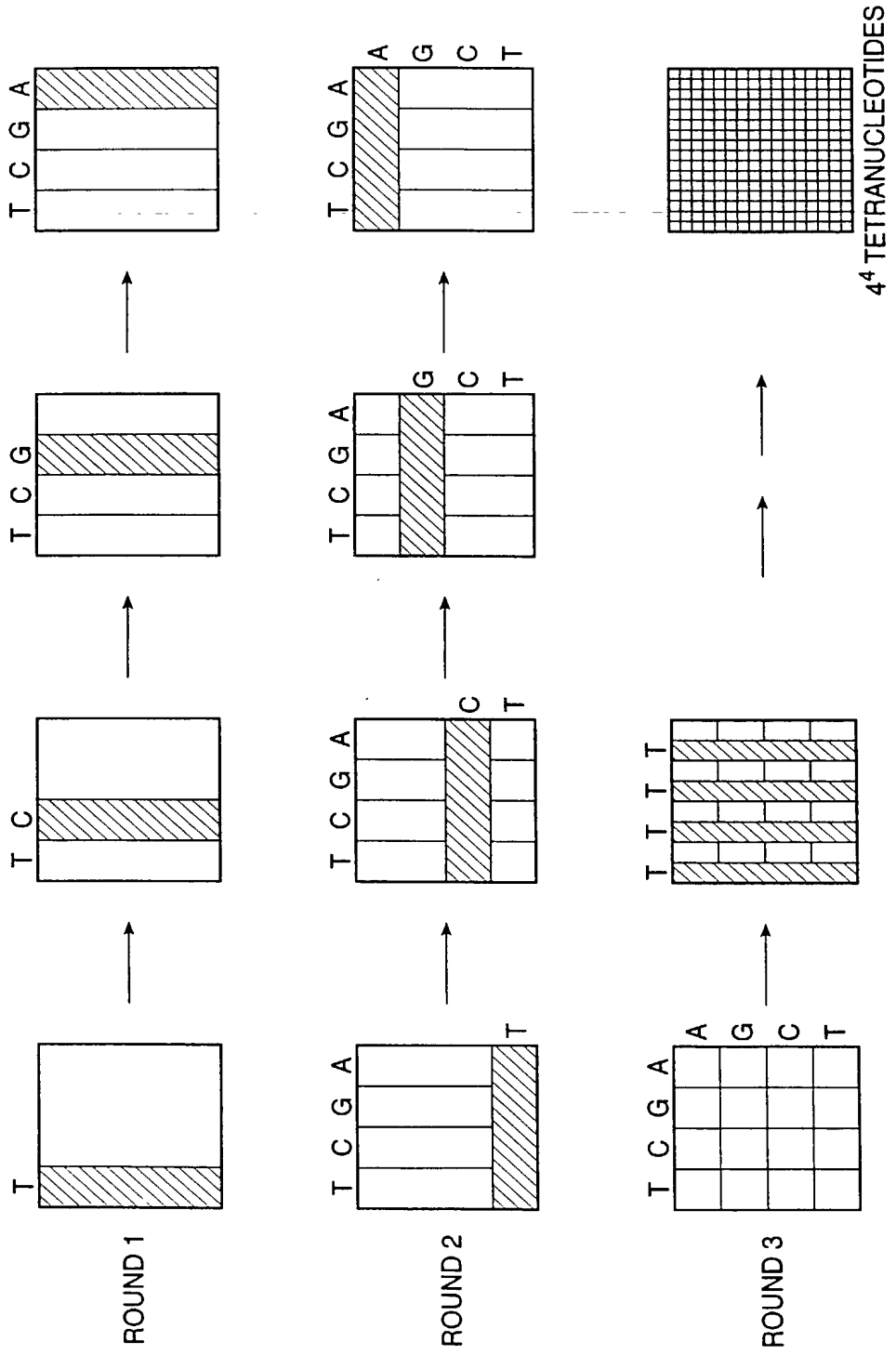


FIG. 4

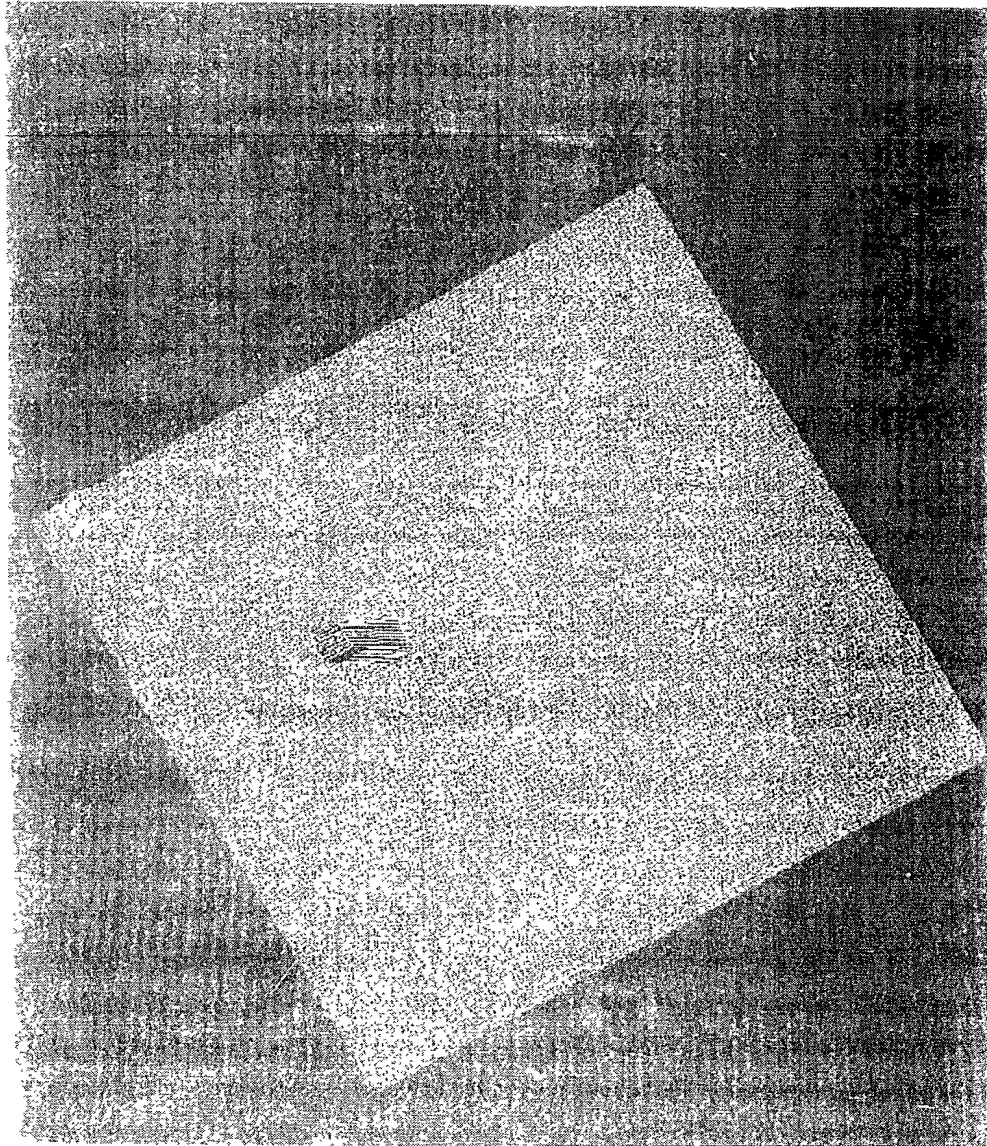


FIG. 5a

Diagram illustrating a quantum communication protocol. A vertical line on the left represents a source. A wavy line extends from it to a circle containing the number 5. To the right of this circle are the letters 'x x y x y' arranged in two rows. Further right is another circle containing the number 3'. To the right of this circle are the letters 'y y x y' arranged in two rows. A large curly bracket on the right groups the top row of letters and the circle 3' under the label 'TARGET'. Another large curly bracket on the right groups the bottom row of letters and the circle 5 under the label 'PROBE'.

A line graph showing the relative binding affinity of the 5'-TGGT-3' sequence for various mismatch positions. The y-axis is labeled 'REL. BINDING AFFINITY' and the x-axis is labeled 'MISMATCH POSITION'. The data points are as follows:

Mismatch Position	Relative Binding Affinity	Sequence
0	1.0	yyxy
1	~0.8	xyxy
2	~0.6	yxxxy
3	~0.6	yyyy
4	~0.8	yyxx

FIG. 6C



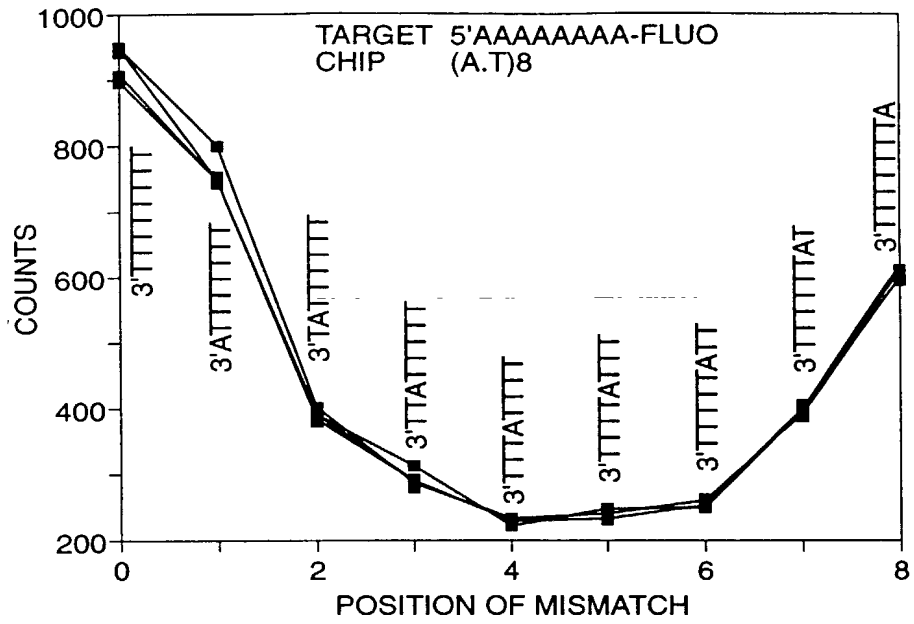


FIG. 8

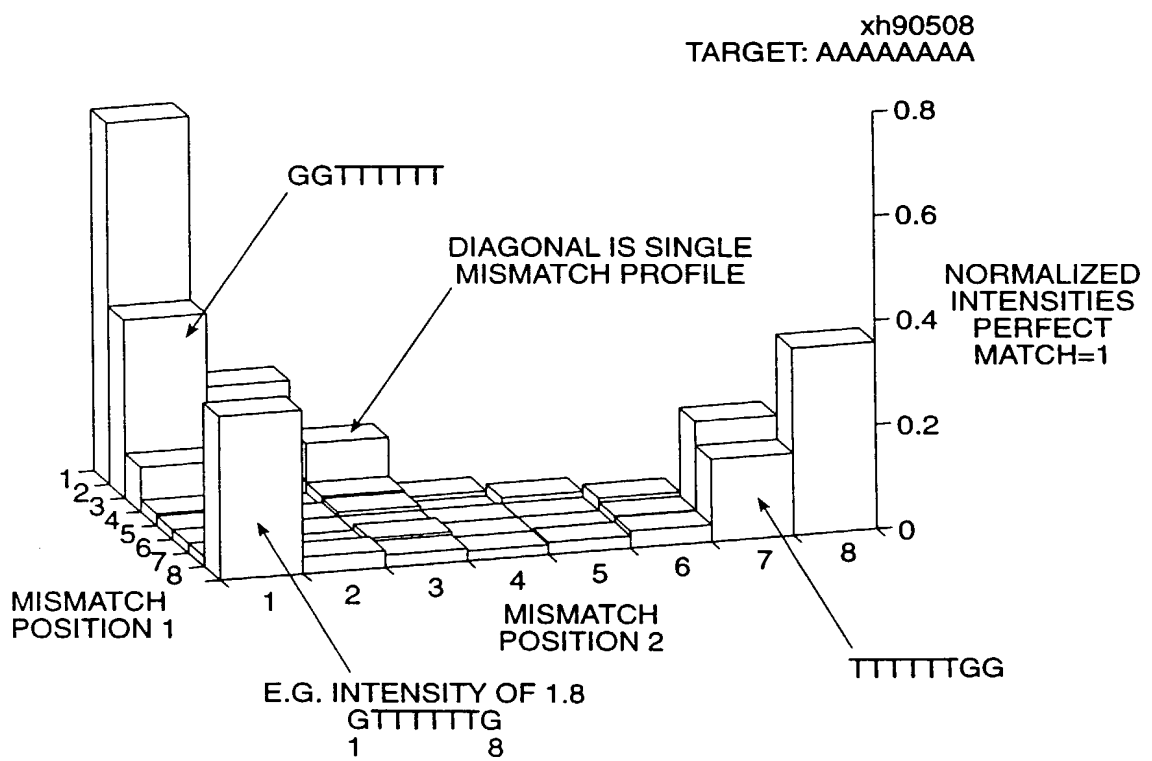


FIG. 9



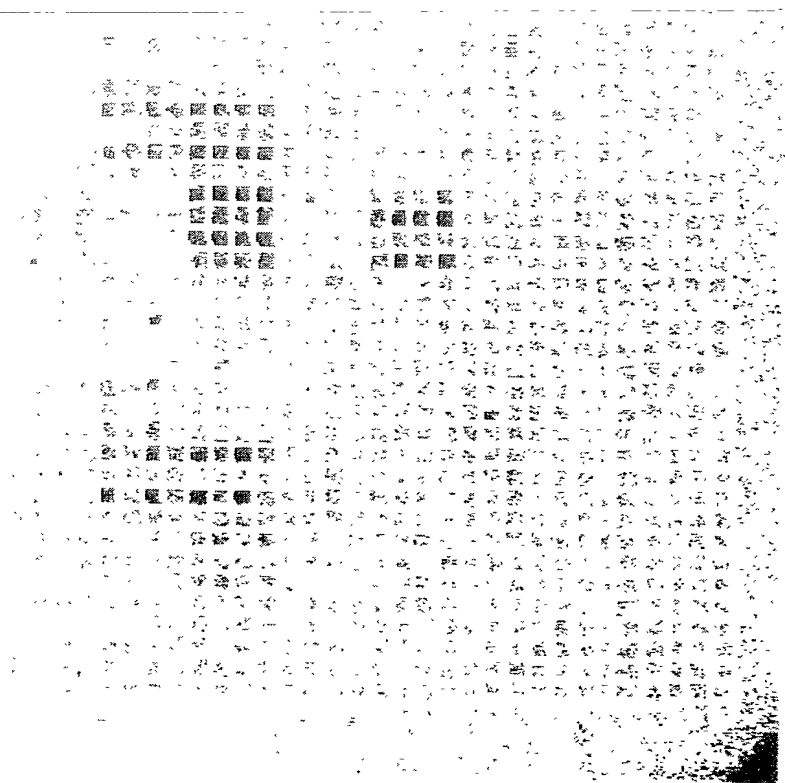


FIG. 10

CHIP: (G-T)<sup>8</sup>  
 TARGET AACCCTAAACCC

GGGTTTGT  
 TGGGTTTG  
 GGGTTTGG

GGGTTTGT 76

GGGTTTGG 180

TGGGTTTG 261  
 MAX INTENSITY

NORMALIZED INTENSITY

MISMATCH POSITION

PERFECT MATCH  $\geq$  NORMALIZED INTENSITY = 1

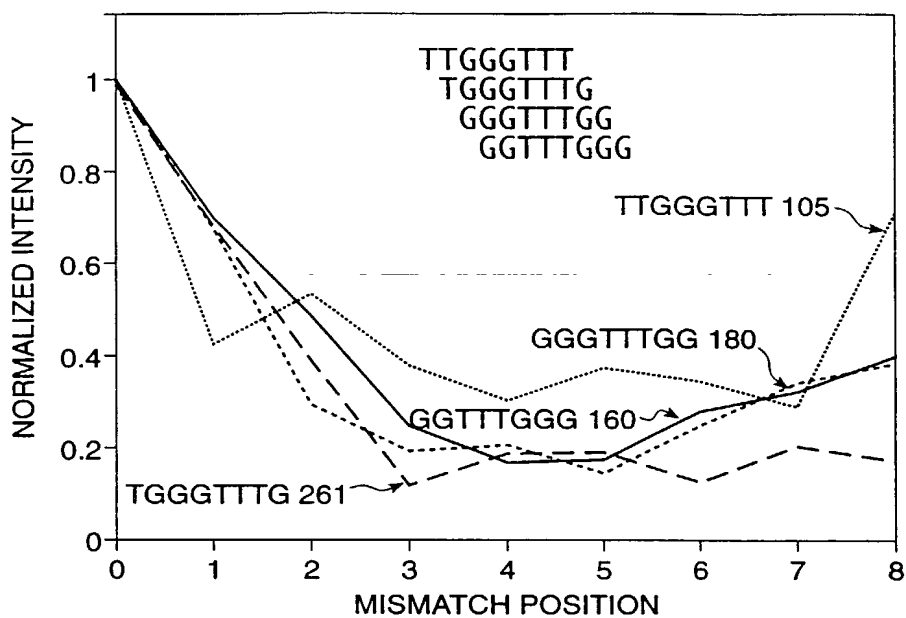


FIG. 11C

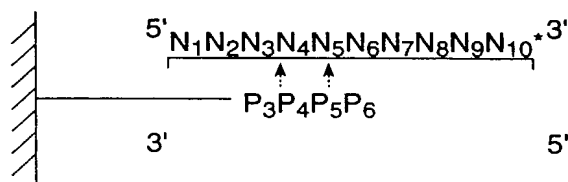


FIG. 12A

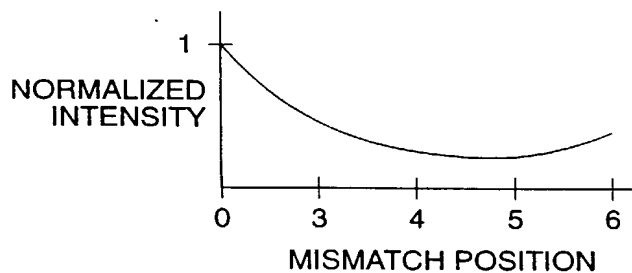


FIG. 12B

Figure 1 displays four dot plots showing the distribution of mismatch positions (0 to 5) for different primer sequences. The sequences are 3'-AP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5', 3'-TP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5', 3'-CP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5', and 3'-GP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5'. Each plot has a y-axis with markers at 1 and 10. The x-axis is labeled 'MISMATCH POSITION'.

- Top Left (3'-AP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5'):** Shows a high frequency of mismatches at position 0 (10 dots) and position 5 (10 dots). Other positions (2, 3, 4) have 2 dots each.
- Top Right (3'-TP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5'):** Shows a high frequency of mismatches at position 0 (10 dots) and position 5 (10 dots). Other positions (2, 3, 4) have 2 dots each.
- Bottom Left (3'-CP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5'):** Shows a high frequency of mismatches at position 0 (10 dots) and position 5 (10 dots). Other positions (2, 3, 4) have 2 dots each.
- Bottom Right (3'-GP<sub>3</sub>P<sub>4</sub>P<sub>5</sub>-5'):** Shows a high frequency of mismatches at position 0 (10 dots) and position 5 (10 dots). Other positions (2, 3, 4) have 2 dots each.

FIG. 12D

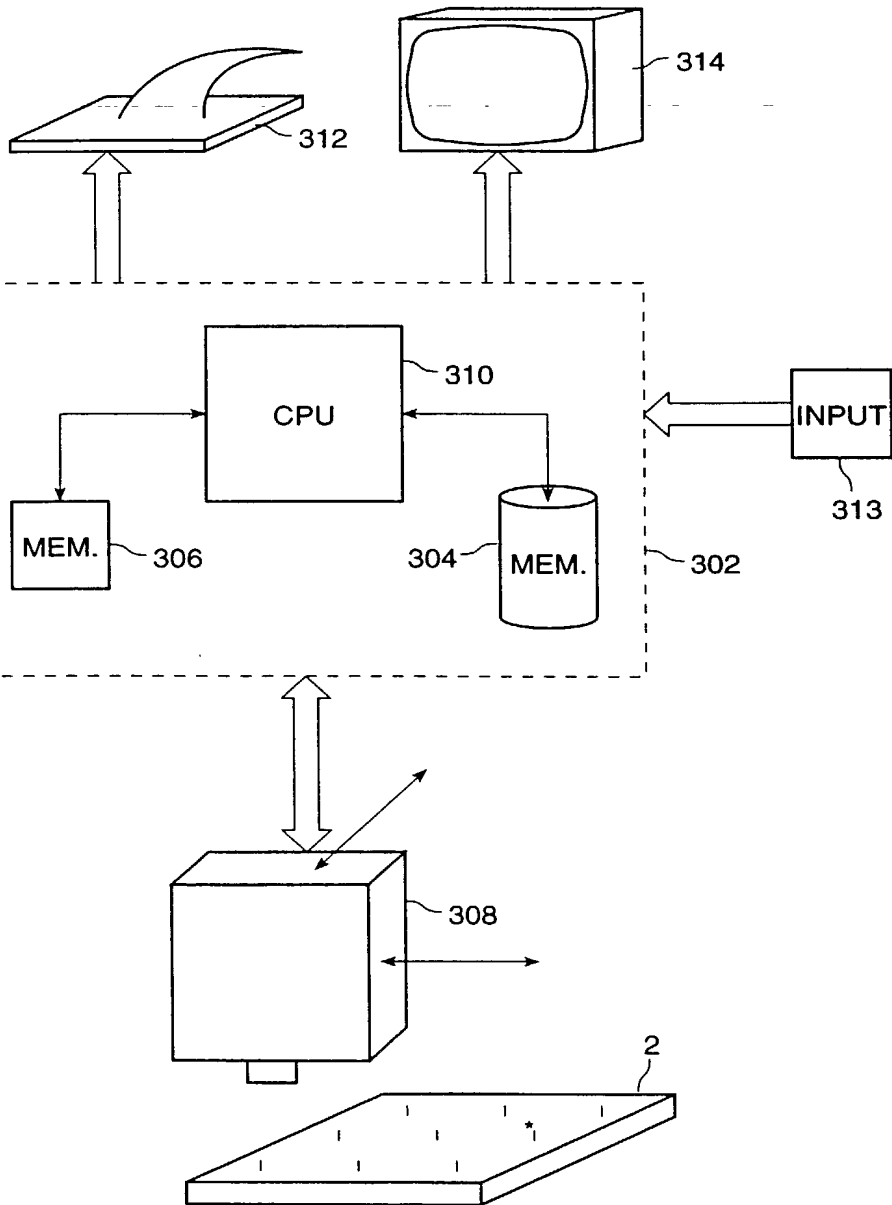


FIG. 13

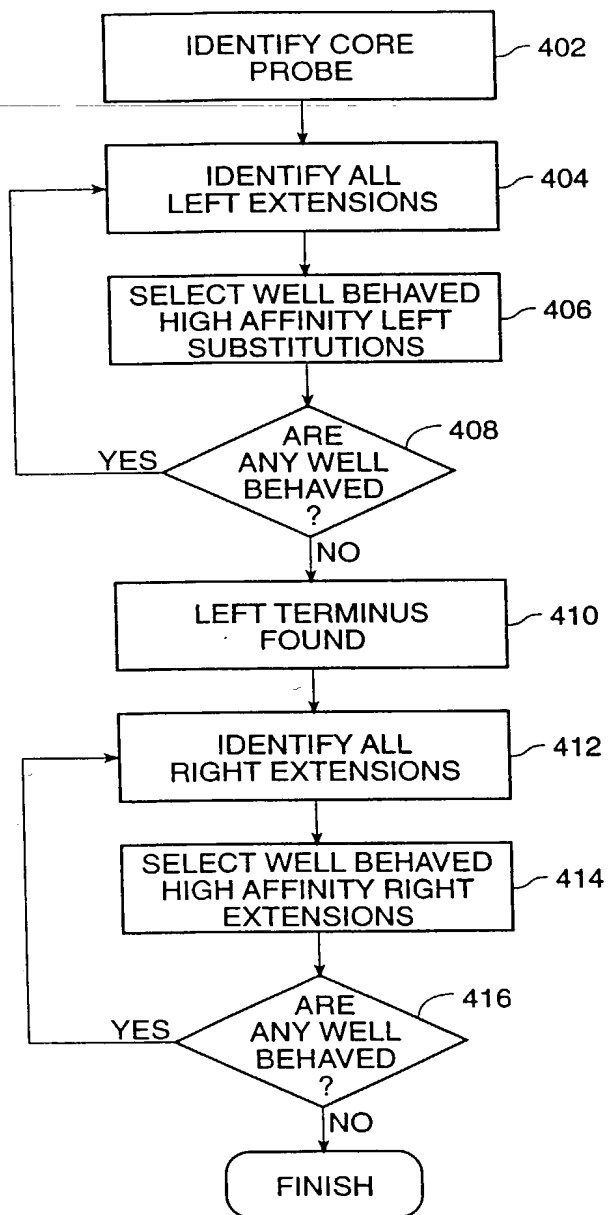


FIG. 14

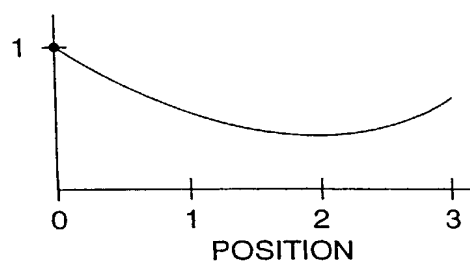


FIG. 15A

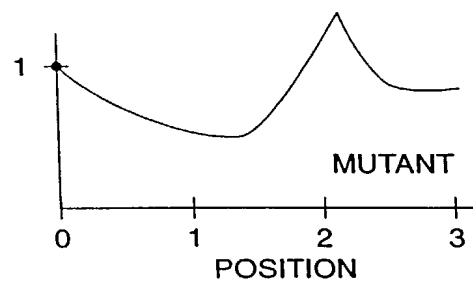


FIG. 15B

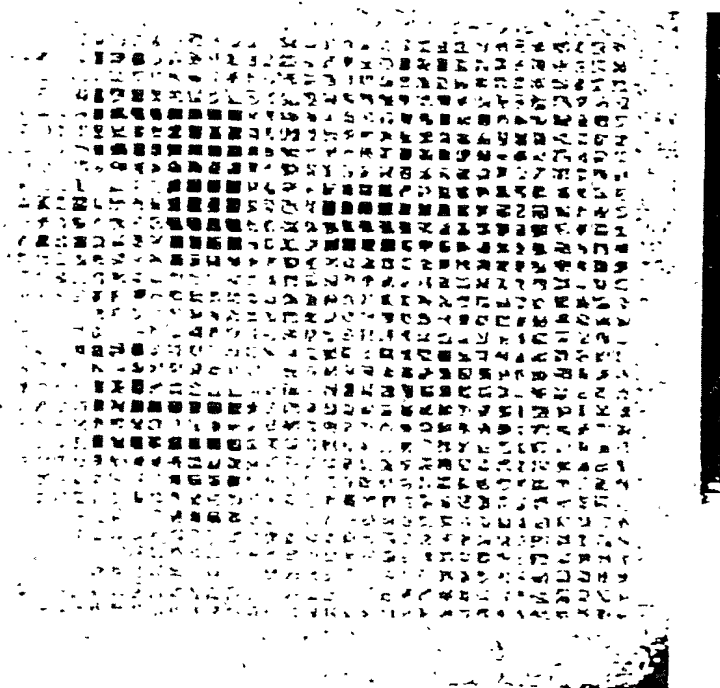


FIG. 16

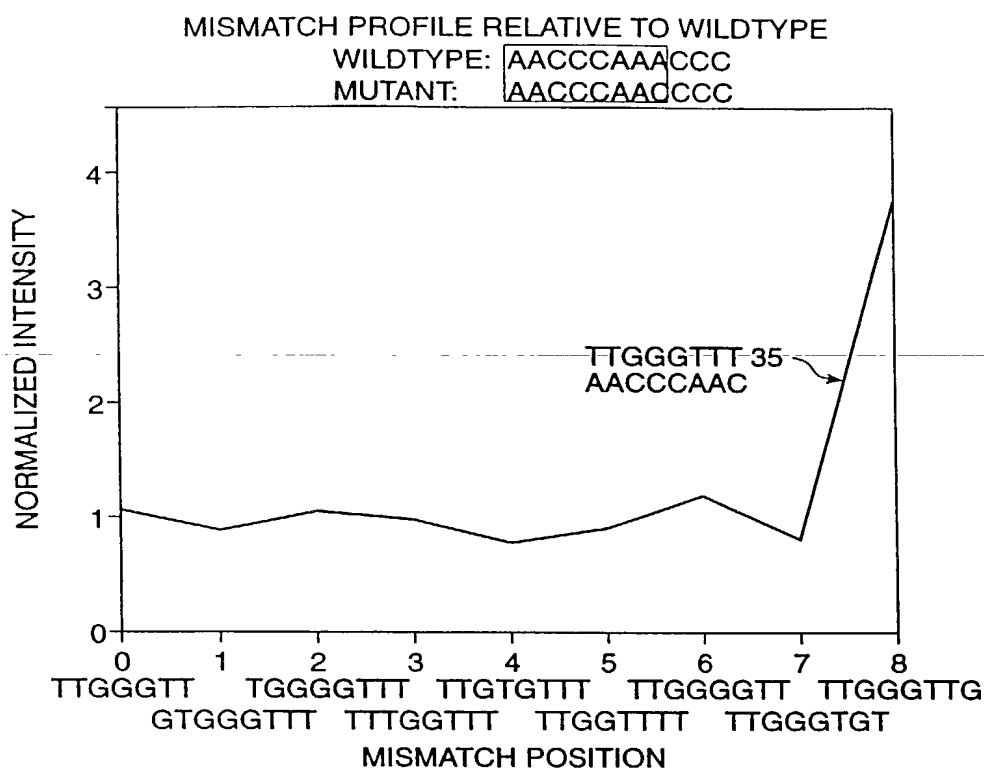


FIG. 17A

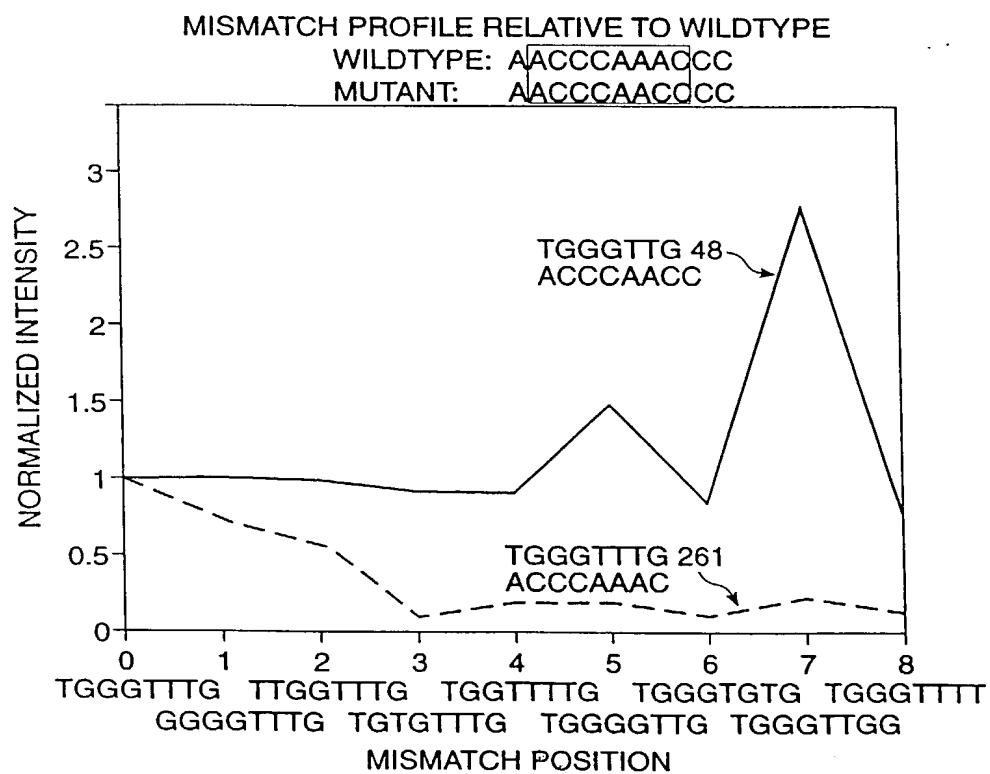


FIG. 17B



CHIP: (G-T)<sup>8</sup> xh91530  
TARGET: AACCCAACCCC